OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: May 22, 2005, 04:54:30 ; Search time 346.363 Seconds
(without alignments)
8744.444 Million cell updates/sec

Title: US-09-763-011D-1
Perfect score: 1851
Sequence: 1 atgtcattagataattcaac........tgttttgaaaaaatagttcg 1851

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match Length	DB	ID	Description
	1	1507.4	81.4	1521	4	US-09-248-796A-5972	Sequence 5972, Ap
	2	983.4	53.1	1257	4	US-09-248-796A-5973	Sequence 5973, Ap
	3	625.4	33.8	816	4	US-09-248-796A-6065	Sequence 6065, Ap
c	4	625.2	33.8	1626	4	US-09-614-221A-521	Sequence 521, App
	5	544.2	29.4	1704	4	US-09-614-221A-534	Sequence 534, App
	6	543.6	29.4	1704	4	US-09-614-221A-96	Sequence 96, Appl
	7	529.2	28.6	1695	4	US-09-614-221A-443	Sequence 443, App
	8	299.4	16.2	417	4	US-09-248-796A-6023	Sequence 6023, Ap
	9	214.4	11.6	243	4	US-09-248-796A-11265	Sequence 11265, A
	10	151.2	8.2	2298	4	US-09-248-796A-5965	Sequence 5965, Ap
c	11	151	8.2	708	3	US-08-998-416-719	Sequence 719, App
	12	144.2	7.8	339	4	US-09-248-796A-5971	Sequence 5971, Ap
c	13	124.6	6.7	1662	4	US-09-248-796A-5975	Sequence 5975, Ap
	14	80.2	4.3	1125	4	US-09-248-796A-6024	Sequence 6024, Ap
	15	72.4	3.9	1960	4	US-09-679-686B-15	Sequence 15, Appl
	16	66.2	3.6	1503	4	US-09-248-796A-5976	Sequence 5976, Ap
	17	64.8	3.5	609	4	US-09-248-796A-6609	Sequence 6609, Ap
	18	59.2	3.2	1659	4	US-09-248-796A-6610	Sequence 6610, Ap
	19	58	3.1	978	4	US-09-248-796A-5978	Sequence 5978, Ap
	20	57	3.1	7218	1	US-08-232-463-14	Sequence 14, Appl
	21	56.6	3.1	612	4	US-09-902-540-1357	Sequence 1357, App
	22	54.2	2.9	474	4	US-09-248-796A-149	Sequence 149, App
	23	51.4	2.8	5227	4	US-09-919-172-79	Sequence 79, Appl
	24	51.4	2.8	5228	4	US-09-919-033-216	Sequence 216, Appl
	25	50.6	2.7	597	4	US-09-248-796A-2683	Sequence 2683, Ap
	26	50.6	2.7	1089	4	US-09-248-796A-150	Sequence 150, App
	27	49.6	2.7	633	4	US-09-248-796A-6030	Sequence 6030, Ap
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c	29	49.4	2.7	405	4	US-09-248-796A-5966	Sequence 5966, Ap
c	30	48.8	2.7	1141	4	US-09-806-708B-214	Sequence 214, App
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c	32	48.2	2.6	614	4	US-09-902-540-1318	Sequence 1318, Ap
c	33	48	2.6	648	4	US-09-248-796A-5974	Sequence 5974, A
c	34	48	2.6	429	4	US-09-248-796A-6022	Sequence 6022, Ap
c	35	47.8	2.6	1137	4	US-09-248-796A-151	Sequence 151, App
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c	37	47.8	2.6	8920	2	US-08-446-855A-1	Sequence 1, Appli
c	38	47.8	2.6	8920	2	US-09-150-741-1	Sequence 1, Appli
c	39	47.2	2.6	832	4	US-09-621-976-2813	Sequence 2813, Ap
c	40	47	2.5	1141	4	US-09-806-708B-22	Sequence 22, Appl
c	41	47	2.5	670689	4	US-09-949-016-12505	Sequence 12505, A
c	42	47	2.5	670690	4	US-09-949-016-14207	Sequence 14207, A
c	43	46.6	2.5	19124	2	US-08-487-826B-13	Sequence 13, Appl
c	44	46.6	2.5	828	3	US-09-998-416-538	Sequence 538, App
c	45	46.2	2.5	2672	1	US-08-703-947-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-248-796A-5972
Sequence 5972, Application US/09248796A
Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1999-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 5972
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-5972

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Qy    193 GGTTTCGATACTGGTACCATTTCTGGTTTCATTAACATGACTGACTTTTTTAGAAAGATTT 252
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Qy    313 GGTTTGTTCAATGTGGTTGTCCCATTGGTGCTGATATG 372
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Db    301 CAAATTGCTTCTCAACATGCTTGGTAT 360
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OM nucleic - nucleic search, using sw model

Run on: May 22, 2005, 05:05:29 ; Search time 1231.07 Seconds
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Scoring table: IDENTITY_NUC
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Searched: 5695437 seqs, 306160638 residues

Total number of hits satisfying chosen parameters: 11390874

Post-processing: Minimum Match 0%
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SUMMARIES

| | | % Query | | | | |
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3	1253	88.9	1653	18	US-10-451-467A-687	Sequence 687, App
4	1253	67.7	1641	18	US-10-451-467A-477	Sequence 477, App
5	1253	67.7	1641	18	US-10-451-467A-551	Sequence 551, App
6	703.6	38.0	1713	17	US-10-369-493-25367	Sequence 25367, App
7	703.6	38.0	2213	18	US-10-451-467A-121	Sequence 121, App
8	702.6	38.0	1713	17	US-10-369-493-25366	Sequence 25366, A
9	702.6	38.0	2213	18	US-10-369-493-25366	Sequence 119, Appli
10	690.8	37.3	1713	17	US-10-112-783A-3	Sequence 3, Appli
11	685	37.0	1704	17	US-10-369-493-25368	Sequence 25368, A
12	685	37.0	2204	18	US-10-451-467A-123	Sequence 123, App
13	678	36.6	1713	17	US-10-312-783A-4	Sequence 4, Appli
14	662	35.8	1683	17	US-10-369-493-45733	Sequence 45733, A
15	657.2	35.5	1713	17	US-10-369-493-45734	Sequence 45734, A
16	625.2	35.5	2213	18	US-10-451-467A-205	Sequence 205, App
17	625.2	33.8	1626	17	US-10-369-493-25554	Sequence 25554, A
18	625.2	33.8	2126	18	US-10-793-639-521	Sequence 521, App
19	602.6	32.6	1725	18	US-10-451-467A-303	Sequence 303, App
20	583.4	31.5	1779	17	US-10-369-493-46000	Sequence 46000, A
21	568.6	30.7	1710	17	US-10-369-493-45814	Sequence 45814, A
22	560.8	30.3	1641	18	US-10-369-493-45560	Sequence 45560, A
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24	544.2	29.4	1704	18	US-10-793-639-534	Sequence 534, App
25	544.2	29.4	1704	17	US-10-369-493-45812	Sequence 45812, A
26	543.6	29.4	1704	18	US-10-369-493-45812	Sequence 45812, A
27	543.6	29.2	1695	17	US-10-369-493-25693	Sequence 25693, A
28	540.4	29.2	1695	18	US-10-369-493-96	Sequence 96, Appl
29	529.2	28.6	1695	17	US-10-369-493-25393	Sequence 25393, A
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31	509.6	27.5	1704	17	US-10-369-493-25230	Sequence 25230, App
32	506.4	27.4	1704	17	US-10-369-493-45897	Sequence 45897, A
33	473.4	25.6	1374	17	US-10-369-493-45759	Sequence 45759, A
34	334.2	18.1	1605	17	US-10-369-493-46317	Sequence 46317, A
35	326.8	17.7	1693	17	US-10-369-493-26276	Sequence 26276, A
36	319.4	17.3	1638	17	US-10-369-493-46318	Sequence 46318, A
37	260.8	14.1	1668	17	US-10-369-493-25715	Sequence 25715, A
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39	254	13.7	1671	17	US-10-369-493-26009	Sequence 26009, A
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45	137.6	7.4	673	18	US-10-653-047-6270	Sequence 6270, Ap

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-10-451-467A-475
Sequence 475, Application US/10451467A
Publication No. US2004016140A1
GENERAL INFORMATION:
   APPLICANT: CONTRERAS, ROLAND HENRI
   APPLICANT: EBERHARDT, INES
   APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
   APPLICANT: REEKMANS, RIEKA JOSEPHINA
   TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
   TITLE OF INVENTION: YEAST AND FUNGI
   FILE REFERENCE: JAB-1667
   CURRENT APPLICATION NUMBER: US/10/451,467A
   CURRENT FILING DATE: 2003-06-19
   PRIOR APPLICATION NUMBER: EP 00870318.3
   PRIOR FILING DATE: 2000-12-22
   PRIOR APPLICATION NUMBER: EP 01870002.1
   PRIOR FILING DATE: 2001-01-04
   PRIOR APPLICATION NUMBER: EP 01870003.9
   PRIOR FILING DATE: 2001-01-09
   NUMBER OF SEQ ID NOS: 732
   SOFTWARE: PatentIn version 3.1
   SEQ ID NO 475
   LENGTH: 1653
   TYPE: DNA
   ORGANISM: Candida albicans
US-10-451-467A-475

Query Match   88.9%; Score 1645; DB 18; Length 1653;
Best Local Similarity 99.7%; Pred. No. 0;
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